

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/542,867
Source: Per
Date Processed by STIC: 2/2/06

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PCT

RAW SEQUENCE LISTING

DATE: 02/02/2006

PATENT APPLICATION: US/10/542,867

TIME: 11:41:17

Input Set : E:\401uspc.app.txt

Output Set: N:\CRF4\02022006\J542867.raw

3 <110> APPLICANT: Shinoda, Tetsuro
 4 Itoyama, Kyo
 5 Hamamura, Tetsuzo
 8 <120> TITLE OF INVENTION: JUVENILE HORMONE ACID METHYLTRANSFERASE
 9 GENES AND METHODS OF USING SAME
 11 <130> FILE REFERENCE: 480230.401USPC
 13 <140> CURRENT APPLICATION NUMBER: US 10/542,867
 C--> 14 <141> CURRENT FILING DATE: 2005-07-20
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00415
 17 <151> PRIOR FILING DATE: 2003-01-20
 19 <160> NUMBER OF SEQ ID NOS: 38
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2890
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Bombyx mori
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (125)..(961)
 31 <223> OTHER INFORMATION:
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 36 tacgaactta aaaaaaaaaa gtgccgacaa atattttatt gcaaaaaaaaa atattaagtc 120
 38 aaaa atg aac aat gca gat tta tac cgc aaa agt aac agc ctc caa aag 169
 39 Met Asn Asn Ala Asp Leu Tyr Arg Lys Ser Asn Ser Leu Gln Lys
 40 1 5 10 15
 42 aga gat gct ctg cgc tgc ctc gag gaa cat gcg aat aag att aag tgg 217
 43 Arg Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp
 44 20 25 30
 46 aaa aaa atc ggt gat aga gtc ata gat ttg ggt tgc gct gac ggt agt 265
 47 Lys Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser
 48 35 40 45
 50 gtt act gat att ttg aaa gtt tac atg cca aaa aat tac gga aga tta 313
 51 Val Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu
 52 50 55 60
 54 gtt ggc tgc gac ata agc gaa gaa atg gtg aaa tac gcg aat aaa cac 361
 55 Val Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His
 56 65 70 75
 58 cac ggc ttc ggt agg act tcg ttc agg gtg ctc gac ata gag ggc gat 409
 59 His Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp
 60 80 85 90 95
 62 ttg acc gca gac ctg aaa caa ggc ttt gat cac gtt ttc tct ttt tac 457
 63 Leu Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr

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64	100	105	110	
66 acc ctc cac tgg atc aga gac cag gaa cga gct ttc cgg aac att ttc				505
67 Thr Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe				
68	115	120	125	
70 aat ctg ctt ggc gac gaa gga gat tgc tta ctt ctg ttc ctg ggc cac				553
71 Asn Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His				
72	130	135	140	
74 act cct atc ttt gat gtt tac cgc aca ctc tcg cat aca gaa aaa tgg				601
75 Thr Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp				
76	145	150	155	
78 cat tct tgg ctc gag cac gtc gat cga ttt ata tca cct tac cat gac				649
79 His Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp				
80 160	165	170	175	
82 aat gaa gat ccc gaa aaa gaa gtt aag aag ata atg gaa aga gtt gga				697
83 Asn Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly				
84	180	185	190	
86 ttt agc aat att gaa gtg caa tgc aaa acg ttg ttc tat gta tac gat				745
87 Phe Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp				
88	195	200	205	
90 gat ttg gat gtt tta aaa aaa tca gta gca gct atc aat cca ttt aat				793
91 Asp Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn				
92	210	215	220	
94 atc ccg aaa gac ata ctt gaa gac ttt tta gaa gat tac ata gat gta				841
95 Ile Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val				
96	225	230	235	
98 gta cgg gag atg agg ctg ctc gac agg tgt aat aac aat gtc ggt gaa				889
99 Val Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu				
100 240	245	250	255	
102 tca gtg tct ata aaa ttt aac tac aaa gtc atc agt gtt tac gcg aga				937
103 Ser Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg				
104	260	265	270	
106 aaa tta tgt tta agt tta atg taa ttaagttaga aaaaaaaaaac aaatccgact				991
107 Lys Leu Cys Leu Ser Leu Met				
108	275			
110 tctaaatctt ggaaataagt ttttttaaca tatttctctc tctttgtctt cccagatttt				1051
112 cgtgattaag ctttctattc actattttta aaagctttct caatatattg aatacagttt				1111
114 agaatacagt tggatatctga aatcactgat ttcgaagtcg gttacttaga acaaatttta				1171
116 ttagttaatt gtattttataa ggaacgctac aatattttatt acagtaagta atttttaaatt				1231
118 tccggaaaca gtggagttca gtggacaatg cagtatcagg agatggctta gatggatgga				1291
120 cgagctcaca gtcacccggt gttaagtggg tactggagcc catagacatc tacaatgtaa				1351
122 atgccgccac cgatatgagt tataaggtct cagaatagct gccccaccct tcaagccgaa				1411
124 acgcgttact gcttcacggc agaaataggc agggcggtgg tacctaccg cgcgactta				1471
126 caagagctcc taccactagt gagagccagc tgctttttgt tgctcgtgtaa aatcggctcg				1531
128 tgtctctagt catatcatag ccgtacaaaa aaatagacaa cttgatatta taactgttct				1591
130 tcaaatttct cgtcacacat acgaaaaata agtttgatgt atttaccgga aatataaatg				1651
132 ttaacatagc tcatatatac atacatata aattcatata tacacattaa gttttaatac				1711
134 tctgaaatat gtctacccca aaacaagaaa gcctactgta ctaaaattgt atgcagtttt				1771
136 agtttttaag tattatttta ataacagtga catctattag cgatacattg aactatttca				1831
138 acacaacatt tttcatatta ttttcctttg aatctaatta ctttttttaa gccgcagtaa				1891

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140 gatggcgggtg ttgtacgact taaagtgttg agaattttaa ataatttcta cggttggttaa 1951
142 attataattg aaatagaaat ccatactatt ttaattactc aactcaacaa ctcaattatt 2011
144 ttttaaagga gatgtgtgag tgagcatcac tagagaattg tttgaccgtt gaccgattgg 2071
146 gctgatttct ttttcattat atccgtaaat tttaggacaa gttttgtacc accaactaca 2131
148 gccactacag tattcattga tttttaatta ccataagttt ggtttgtgta aagtatatatt 2191
150 ataataacga taaatttggg ttgagtcgtg atagttggac atttcaacta gtccgcttgc 2251
152 tcatttgatt atactatgtg cttagtgcgg gttcttttac gctatcgaga acgttaaaga 2311
154 actcgacta agcacactat tgtattttat ttgttgcaca aatatattta gaaacaatcg 2371
156 tgtataatca tcatgcttta aaagtattcc tataaaatca taaacagtca caaaatttat 2431
158 ttttagtgag aattacatga aacaaattat gaaacaaagt ttgattatac tttcaaagt 2491
160 ttcattactg tttttaagct taaggataaa aatggcatgt ttgtgtgttt actcaggccc 2551
162 taagcaacac gcgttggctt ttaagtaaac tttgaagtct tagttattcc tggggtttatt 2611
164 tggcacgtta gtaaaatcta ccctgccatt tagtaccatt agagtgcgaa tgattacagc 2671
166 gtatgattat tgtttacatt ttttaatttt gttaattact taacgaaacc tgccccggat 2731
168 ttattgacaa cataattagt aaaacatgtg ataatttgaa caatgacaaa tttattgtta 2791
170 gttaatttat ttcactttgt atataataat tgtaagtgtg atgtttaaat aaataaaaact 2851
172 aaagtgtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2890

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175 <210> SEQ ID NO: 2

176 <211> LENGTH: 278

177 <212> TYPE: PRT

178 <213> ORGANISM: Bombyx mori

180 <400> SEQUENCE: 2

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182 1 5 10 15
184 Asp Ala Leu Arg Cys Leu Glu Glu His Ala Asn Lys Ile Lys Trp Lys
185 20 25 30
187 Lys Ile Gly Asp Arg Val Ile Asp Leu Gly Cys Ala Asp Gly Ser Val
188 35 40 45
190 Thr Asp Ile Leu Lys Val Tyr Met Pro Lys Asn Tyr Gly Arg Leu Val
191 50 55 60
193 Gly Cys Asp Ile Ser Glu Glu Met Val Lys Tyr Ala Asn Lys His His
194 65 70 75 80
196 Gly Phe Gly Arg Thr Ser Phe Arg Val Leu Asp Ile Glu Gly Asp Leu
197 85 90 95
199 Thr Ala Asp Leu Lys Gln Gly Phe Asp His Val Phe Ser Phe Tyr Thr
200 100 105 110
202 Leu His Trp Ile Arg Asp Gln Glu Arg Ala Phe Arg Asn Ile Phe Asn
203 115 120 125
205 Leu Leu Gly Asp Glu Gly Asp Cys Leu Leu Leu Phe Leu Gly His Thr
206 130 135 140
208 Pro Ile Phe Asp Val Tyr Arg Thr Leu Ser His Thr Glu Lys Trp His
209 145 150 155 160
211 Ser Trp Leu Glu His Val Asp Arg Phe Ile Ser Pro Tyr His Asp Asn
212 165 170 175
214 Glu Asp Pro Glu Lys Glu Val Lys Lys Ile Met Glu Arg Val Gly Phe
215 180 185 190
217 Ser Asn Ile Glu Val Gln Cys Lys Thr Leu Phe Tyr Val Tyr Asp Asp
218 195 200 205
220 Leu Asp Val Leu Lys Lys Ser Val Ala Ala Ile Asn Pro Phe Asn Ile

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221      210      215      220
223 Pro Lys Asp Ile Leu Glu Asp Phe Leu Glu Asp Tyr Ile Asp Val Val
224 225      230      235      240
226 Arg Glu Met Arg Leu Leu Asp Arg Cys Asn Asn Asn Val Gly Glu Ser
227      245      250      255
229 Val Ser Ile Lys Phe Asn Tyr Lys Val Ile Ser Val Tyr Ala Arg Lys
230      260      265      270
232 Leu Cys Leu Ser Leu Met
233      275
236 <210> SEQ ID NO: 3
237 <211> LENGTH: 938
238 <212> TYPE: DNA
239 <213> ORGANISM: Drosophila melanogaster
241 <220> FEATURE:
242 <221> NAME/KEY: CDS
243 <222> LOCATION: (1)..(894)
244 <223> OTHER INFORMATION:
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247 atg aat cag gcc tct cta tat cag cac gcc aac cag gtg caa agg cac      48
248 Met Asn Gln Ala Ser Leu Tyr Gln His Ala Asn Gln Val Gln Arg His
249 1      5      10      15
251 gat gcc aaa ttg att ctg gat gag ttc gca tcg acc atg cag tgg cga      96
252 Asp Ala Lys Leu Ile Leu Asp Glu Phe Ala Ser Thr Met Gln Trp Arg
253      20      25      30
255 tcc gat gga gag gat gcc ctc ctg gat gtg ggt tca gga tct ggt aac      144
256 Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn
257      35      40      45
259 gtg ctc atg gac ttt gta aag cca ctg ctc ccg att cgt gga caa ctg      192
260 Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
261      50      55      60
263 gtg ggc aca gac atc tcc agc cag atg gtg cac tat gcc agt aag cat      240
264 Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
265 65      70      75      80
267 tac cag cga gag gag cgt acc aga ttc cag gtt ctg gac att gga tgc      288
268 Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys
269      85      90      95
271 gaa cgg ctg ccc gag gag ctg agc ggc aga ttt gac cat gtc acc tcg      336
272 Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser
273      100      105      110
275 ttc tac tgc ctc cat tgg gtg caa aat ctg aaa gga gct ctc gga aat      384
276 Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn
277      115      120      125
279 atc tac aat ctt ctg aag ccc gaa ggt ggc gac tgc ctc ctg gca ttt      432
280 Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe
281      130      135      140
283 ttg gcc tcc aat ccg gtt tac gaa gtc tat aag att ctt aaa acg aat      480
284 Leu Ala Ser Asn Pro Val Tyr Glu Val Tyr Lys Ile Leu Lys Thr Asn
285 145      150      155      160
287 gac aag tgg tcg act tat atg cag gat gtg gag aac ttc ata tcc cca      528

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288 Asp Lys Trp Ser Thr Tyr Met Gln Asp Val Glu Asn Phe Ile Ser Pro
289           165           170           175
291 ctt cac tac agt cta aat cct ggc gag gaa ttc agc cag ttg ttg aac      576
292 Leu His Tyr Ser Leu Asn Pro Gly Glu Glu Phe Ser Gln Leu Leu Asn
293           180           185           190
295 gat gtg ggt ttc gtg caa cac aat gtg gaa att cga aac gaa gtg ttt      624
296 Asp Val Gly Phe Val Gln His Asn Val Glu Ile Arg Asn Glu Val Phe
297           195           200           205
299 gtt tat gaa ggt gta agg act ctg aaa gat aat gta aag gcc att tgt      672
300 Val Tyr Glu Gly Val Arg Thr Leu Lys Asp Asn Val Lys Ala Ile Cys
301           210           215           220
303 cct ttt ctt gag cga atg cct gca gat ttg cat gaa cag ttc ctg gat      720
304 Pro Phe Leu Glu Arg Met Pro Ala Asp Leu His Glu Gln Phe Leu Asp
305 225           230           235           240
307 gac ttc ata gac att gtt ata tcc atg aat ttg cag caa ggt gaa aat      768
308 Asp Phe Ile Asp Ile Val Ile Ser Met Asn Leu Gln Gln Gly Glu Asn
309           245           250           255
311 aat gag gat caa aag ttc cta tct ccc tat aaa ctg gtg gtg gcc tat      816
312 Asn Glu Asp Gln Lys Phe Leu Ser Pro Tyr Lys Leu Val Val Ala Tyr
313           260           265           270
315 gct cgc aag act cct gaa ttt gtg aat aat gtt ttc ctg gag cct aca      864
316 Ala Arg Lys Thr Pro Glu Phe Val Asn Asn Val Phe Leu Glu Pro Thr
317           275           280           285
319 cat caa aac ttg gtt aag gga ata aat taa ttttatttta caaattaaca      914
320 His Gln Asn Leu Val Lys Gly Ile Asn
321           290           295
323 gtaattgcat ttgttaacag agtc      938
326 <210> SEQ ID NO: 4
327 <211> LENGTH: 297
328 <212> TYPE: PRT
329 <213> ORGANISM: Drosophila melanogaster
331 <400> SEQUENCE: 4
332 Met Asn Gln Ala Ser Leu Tyr Gln His Ala Asn Gln Val Gln Arg His
333 1           5           10           15
335 Asp Ala Lys Leu Ile Leu Asp Glu Phe Ala Ser Thr Met Gln Trp Arg
336           20           25           30
338 Ser Asp Gly Glu Asp Ala Leu Leu Asp Val Gly Ser Gly Ser Gly Asn
339           35           40           45
341 Val Leu Met Asp Phe Val Lys Pro Leu Leu Pro Ile Arg Gly Gln Leu
342           50           55           60
344 Val Gly Thr Asp Ile Ser Ser Gln Met Val His Tyr Ala Ser Lys His
345 65           70           75           80
347 Tyr Gln Arg Glu Glu Arg Thr Arg Phe Gln Val Leu Asp Ile Gly Cys
348           85           90           95
350 Glu Arg Leu Pro Glu Glu Leu Ser Gly Arg Phe Asp His Val Thr Ser
351           100          105          110
353 Phe Tyr Cys Leu His Trp Val Gln Asn Leu Lys Gly Ala Leu Gly Asn
354           115          120          125
356 Ile Tyr Asn Leu Leu Lys Pro Glu Gly Gly Asp Cys Leu Leu Ala Phe

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 6,15
Seq#:20; N Pos. 6,12
Seq#:29; Xaa Pos. 2,3,5,7
Seq#:30; Xaa Pos. 5,8,9,13
Seq#:31; Xaa Pos. 1,4
Seq#:32; Xaa Pos. 1,3,10
Seq#:33; Xaa Pos. 9
Seq#:34; Xaa Pos. 2,5,8
Seq#:35; Xaa Pos. 4
Seq#:36; Xaa Pos. 4

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34
Seq#:35,36

VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31
L:246 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:244
L:400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:398
L:545 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:543
L:695 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:693
L:957 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:979 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
L:1140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:1258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:1276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0